



(1) GENERAL INFORMATION:

- (i) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie
- (ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: David Prashker, Esq.
(B) STREET: P.O. Box 5387
(C) CITY: Magnolia
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 01930
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
(B) COMPUTER: IBM PS/1
(C) OPERATING SYSTEM: MS DOS
(D) SOFTWARE: WordPerfect version 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/145,916
(B) FILING DATE: September 2, 1998
(C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: David Prashker, Esq.
(B) REGISTRATION NUMBER: 29,693
(C) REFERENCE/DOCKET NUMBER: BIS-039
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60
CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCGTGAAGACC AAGATGGCTC TGGGGACGAC 120
TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACAAGCTCC CAGTCACCCA ACAGGCCTCA 420
ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTACGT CTCATCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCAGCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAGAGG TTGTGGAGGA TGAACTACC 600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAGG AA 762

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180
CCCCTAAACT TCTGCCGTAG CTCCCTTCA AGCCAGCGAA TTTATTCTTT AAAACCAGAA 240

ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
 AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
 AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
 AGGAAGCGAG CGCCCCCGAG CCCCCGAGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
 GGTACTCTGC TCCGGATTCC TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
 TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
 TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCCTGTCGG CGGAGTCGAG AGCAGAGCTG 660
 ACATCTGATA AAGACATGTA CTTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
 CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
 AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTGACTAG TGCTGCTCCA 840
 AAAGTGGAAA CCACGACGCT GAATATACAC AACAAGATAC CTGCTCAGAC AAAGTCACCT 900
 GAAGAAACTG ATAAAGAGAA AGTTCACTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
 1 5 10 15
 Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
 20 25 30
 Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
 35 40 45
 Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
 50 55 60
 Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
 65 70 75 80
 Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
 85 90 95
 Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
 100 105 110
 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
 115 120 125
 Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
 130 135 140
 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
 145 150 155 160
 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
 165 170 175
 Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
 180 185 190
 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
 195 200 205
 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
 210 215 220
 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
 225 230 235 240
 Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
 245 250 255
 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
 260 265 270
 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
 275 280 285
 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Thr Asp
 290 295 300
 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
 305 310 315 320
 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
 325 330 335

Sub
 B1
 cont
 A3
 Cont

Lys Arg Thr Glu
340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCGCGGAG CTGCGGCGCC 60
TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
AGAACTACGA GAGGCCCGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
TGGAGACAGC GGTACAGCTC ACCACGGACA CGTCCGTCCC ACTGCCCCACC ACGGTGGCCG 300
TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
ACACGTCCCC TGAGCAAAGA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
TGATCCCCAG CTGGAAGACA ACCACGCCA GTACCACTGC CAGTGAATCC CCCAGTACCA 480
CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
CTGTGGCCAC CTCCAAGCCG ACCACTACCC AGAGGTTCCT GCCCCCCTTT GTCACCAAGG 600
CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCACCAC CTCCATCCCT GAAACCAAGT 660
TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
TGCCAAAACC AAGCACTTCC AGGACTGCAG AATCCACGGA AAAAAGCACT GCCTTGCTT 780
CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
CACCACCAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
GCCCCAGGGC AGTCGATTCG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
AGATACTTCT CTGGAGCCCT CCCGACGAT GAAGACGCTG GGGGCCCTGA GCAGGACTCT 180
GACTTTGAGC TGTGCGGTTT CCGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
ATCCGTGTCC CCTCAGAGCC CAAGGAAGTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCAG 420
GGCAGCAACA TTTTGAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCGGAGA TCTCGGGAGA GCACCTGCGG 180
ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAATGG AGGAGAACCT GGCCAACCAC 240
AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
ACACTGCAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540

CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCAGTGGCG 600
 CCGTTTGGGG ATGCCCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
 CGATCCTTTG TGCAGGGGCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
 CCTCTGGCCC CAGAATGTTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
 GGAGTCCCTG GTGCCCCGGC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
 GAGGCCAAGG CCCAGTCCG AGACATTGAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
 TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260
 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCTT 1320
 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
 GCCAGTGATG ACGGCAGTGG CTCGGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
 CGGAGGGTCA GCAAGAAGAG CTCGAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560
 TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
 1 5 10 15
 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 20 25 30
 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
 65 70 75 80
 Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
 85 90 95
 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
 100 105 110
 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
 115 120 125
 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
 130 135 140
 Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
 145 150 155 160
 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
 165 170 175
 Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
 180 185 190
 Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu
 195 200 205
 Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
 210 215 220
 Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
 225 230 235 240
 Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
 245 250 255
 Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys
 260 265 270
 Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala
 275 280 285
 Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe

See
 B1
 cont
 23
 cont

290 295 300
 Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser Val His Met Trp
 305 310 315 320
 Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr
 325 330 335
 Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro His Gly
 340 345 350
 Ser Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Leu Gln Glu
 355 360 365
 Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala
 370 375 380
 Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu Pro Gly Thr Leu
 385 390 395 400
 Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp
 405 410 415
 Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly
 420 425 430
 Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys
 435 440 445
 Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr
 450 455 460
 Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp
 465 470 475 480
 Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp
 485 490 495
 Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Ser Arg Thr
 500 505 510
 Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys
 515 520 525
 Thr Ser Ala
 530

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60
 GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60
 CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
 1 5 10 15

Sub
 B1
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 23
 Cont

Ile Phe Leu Ile Leu Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTTCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60
GCTGCAGCCA GGCCAGGTG GCGTAACTG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Thr Arg Pro Glu Pro His Tyr Phe Phe Leu Leu Phe Leu Phe Thr
1 5 10 15
Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
20 25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid

Sub
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A3
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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCCCACCA ACGAGTTCTA CGCATGA 87

